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5 | L41870 Homo sapiens retinoblastoma
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6 | A01444 H. sapiens DNA for 4.6 k
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8 | M15400 Homo sapiens retinoblas
1 | M2531 Human mutated retinoblas
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1 | M2528 Human retinoblastoma sus
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Dryja,T.P. and Friend,S.
Human DNA in the diagnosis of retinoblastoma
Patent: EP 0259031-A2 1 09-MAR-1988;
Location/Qualifiers
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8 Human retinoblastoma
2 Homo sapiens retinobl
6 Homo sapiens retinobl
6 Homo sapiens retinobl
5 Sequence 18 from Pate
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451 1515	435 ysalaleuGluvalValMetAlaThrTyrSerArgSerThrSerGlnAsn 
435 1465	418 nPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaC 
418 1415	402 ValMetGluSerMetLeuLysSerGluGluGluArgLeuSerIleGlnAs 
401 1365	385 algluileglySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArg 
385 1315	368 eGlyTyrileDheLysGluLysDheAlaLysAlaValGlyGlnGlyCysV 
368 1265	ASNCYSTHIVALASNPTOLYSGIUSETIIELEULYSAIGVALLYSASPII 
351 1215	335 euasnSeralaSeraspGlnProSerGluasnLeuIleSerTyrPheasn 
335 1165	318 sThrProValArgThrValMetAsnThrIleGlnGlnLeuMetMetLleL 
318 1115	302 ThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHi 
301 1065	285 isasplysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 
285 1015	268 uGluileTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspH  }
268 965	252 ValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyrGl 
251 915	ysasnvalTyrPheLysasnDheIleProPheMetAsnSerLeuGlyLeu 
235 865	218 gIleileGluValLeuCysLysGluHisGluCysAsnIleAspGluValL
218 815	202 GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGluAsnAspThrAr 
201 765	185 yrlysthralaVallieProlleAsnGlySerProArgThrProArgArg
185 715	168 lleuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProT 
168 665	152 LeuGlnMetGluAspAspLeuVallleSerPheGlnLeuMetLeuCysVa 
615	566 TGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGGAAGTA

735 roTyrLysPheProSerSerP 	718 aSerThrargProProThrLe	702 TyrAsnSerValPheMetGln                  2266 TATAACTCGGTCTTCATGCAG	685 heLysargValleuileLysg                    	668 SILEILEVALTHIALATYILYS 	652 CysSerMetTyrGlyIleCys	635 lnAsnGluTyrGluLeuMetA 	618 uHiSProGluLeuGluHiSI1 	602 ArgLeuAlaTyrLeuArgLeu 	585 lnLysProLeuLysSerThrS 	568 lasnSerThralaasnalag1 	552 TyrLeuSerProValArgSer 	535 laCysProLeuAsnLeuProL 	518 uIleLysGlnSerLysAspAr 	502 ArgīleMetGluSerLeuAla 	485 luGlyAsnLeuThrArgGluM 	468 nLeulysalaPheAspPheTy 	452 LeuAspSerGlyThrAspLeu 
roLeuArgileProGlyGlyAsnileTyr                  CTTACGGATTCCTGGAGGGAACATCTAT	uSerProlleProHislleProArgSerP	ArgLeuLysThrAsnIleLeuGlnTyrAl . 	lugluglutyraspserilerlevalphe	ASPLeuProHisalavalGlnGluThrP                 ATCTTCCTCATGCTGTTCAGGAGACAT	LysValLysAsnIleAspLeuLysPheLy (	rgasparghisleuaspGlnIlemetmet (	elleTrpThrLeuPheGlnHisThrLeuG (	ASNThrLeuCySGluArgLeuLeuSerGl (	erLeuSerLeuPheTyrLysLysValTyr                     CTCTTTCACTGTTTTATAAAAAGTGTAT	uThrGlnAlaThrSerAlaPheGlnThrG : 	ProLysLysClySerThrThrArgVa (	euGlnAsnAsnHisThrAlaAlaAspMet ! 	gGluGlyProThrAspHisLeuGluSerA	TrpLeuSerAspSerProLeuPheAspLe	etilelyshisleuGluargCysGluhis 	TLYSVALI1eGluSerPheI1eLySAlaG	SerPheProTrpIleLeuAsnValLeuAs 4
751 2415	735 2365	718 2315	701 2265	685 2215	668 2165	651 2115	635 2065	618 2015	601 1965	585 1915	568 1865	551 1815	535 1765	518 1715	1665	485 1615	468 1565

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ACCESSION J
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FEATURES
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ORIGIN
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US-09-026-459A-31 x I81465
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LOCUS 181465
                                                                                                                                                     Quality: 873.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                     Align seg 1/1 to: 181465 from: 1 to: 2994
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                  35 lyGlyTyrIleGlnLysLysLysGluLeuTrpGlyIleCysIlePheIle 51
                                                                                                                                                                                                     Unknown.
Unknown.
Unclassified.
1 (bases I to 2994)
1 (bases I to 2994)
1 Shepard, H. Michael and Wen, S. Fen.
Characterization of a novel anti-p110.sup.RB monoclonal antibody
Patent: US 5710255-A 2 20-JAN-1998;
Location/Oualifiers
1. 2994
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                                                                                                                                                                                                                                                                                                                                                      181465 2994 bp DNA
Sequence 2 from patent US 5710255.
181465 1GI:3209762
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Gaps: 0
Percent Identity: 100.000
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| 1111| 1114| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 1111| 111| 1111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 111| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 11| 1
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                              seq_documentation_block:
LOCUS HUMRBLMRAA 4839 bp mRNA
DEFINITION Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA
                                                                                                                                                                                                                                                                                                             seq_name: gb_pr2:HUMRB1MRNA
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                                                         L41870,1 GI:793994
retinoblastoma protein; retinoblastoma susceptibility.
Homo sapiens cDNA to mRNA.
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
McGee, T.L., Yandell, D.W. and Dryja, T.P. Structure and partial genomic sequence of the human retinoblastoma
                                                                                                                                                                                                               mutations.
                                          (sites)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS	NOI		44444000000000000000000000000000000000		Doc:11+
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TOGGICTICAT ACAGAGACTAGAGACATATATATATATATATATATATATA	1912 ACAITCAMACGIGIIIIAGA CAMAAAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG		1804 AGGCATTTGGACCAAATTATGATGTTCCALGIA DE AGGCATTATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT	1/4 CARATCARCTIGUACCCTTTCCAGCACACCCCTGCAGAATGAGATA GAACTCATGAGAGACCCTTTCCAGCACACCCCTGCAGAATGAGTATGAACTCATGAGAGACACCCTGCAGAATGAGTATGAACTCATGAGAGACACCCTGCAGAATGAGTATGAACTCATGAGAGACACCCTGCAGAATGAGACTATGAACTCATGAGAGACACCCTGCAGAATGAGACTATGAACTCATGAGAGACACCCTGCAGAATGAGAACTCATGAACGAATATATA	1684 GCCTATCT	Oy 1624 ACCCAGAAGCCATTGAAATCTACCTCTTTTCACTGTTTTATAAAAAAGTGTATCGGCTA 1683	Qy 1564 TCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACCAAGCCACCTTCCAG 1823	ANTANTOACROTGCASCASCATATGTATCTTTGTCCTGTAAGATCTCCAAGCAAAAAGGT	GACCGAGAAGGACCAACTGATCACCTTGAATCTGCTCTTTTAATCTTCCTCTCCAG [			1264 CTGAATGT	1204 TARAGCAGAAGTACATCTGCAGAATCTTGCATTCTGCAGTACAGTTTGTCTTTCCCAGGAGTT  14111111111111111111111111111111111	11111111111111111111111111111111111111	104 GANTCCATGCTTAGATCAGAAGAAGAAGATTATCCATTCAAAATTTTAGCAAACTTCTG 1372 GAATCCATGCTTAAATCAGAAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCTG 1374 AAAGAAACATTTTTAGATATCATATTTTAGCGTGCGCGCGC	1024 TGTGTCGI           1312 TGTGTCGI	Qy 964 AGAGTGAAGGATATAGGATACATCTTTAAAGAGAAAATTTGCTAAAGCTGTGGGACAGGGT 1023	Qy 904 GAAAATCTGATTTCCTATTTTAACAACTGCACTGGACTCGAAAGAAA

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Ouery Match  99.9%; Score 2493; DB 5; Length 2994;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Matches 2493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 4 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTT 63  LILLIHILIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH	RESULT 2  IB1465  IB1465  IB1465  DEFINITION Sequence 2 from patent US 5710255.  ACCESSION IB1465.1 GI:3209762  KEYWORDS SOURCE Unknown. ORCOSH Unknown. ORCOSH Unknown. AUTHORS TITLE Unknown. JOURNAL Patent: US 5710255 A 2 20-JAN-1998; FEATURES Source Location/Qualifiers Source JOSPAN BASE COUNT 974 a 618 c 593 g 809 t	Db 2272 TCGGTCTTCATGCAGAGACTGAAAACAAATATTTGCAGGTATGCTTCCACCAGGCCCCTT 2331  Qy 2044 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCACCAGGCCCCTTA 2103  Db 2332 ACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCACAGTTCACCAGTTCACCCTTA 2391  Qy 2104 CGGATTCCTGGAGGAACATCCTCACATTCCACCAAGAGCCCTTACAAGATTCCACAGTTCCACCATTCCACAAAATTCCACAAGAAGCCCTTACAAAATTCCACAAAAATTCCACAAAAATTCCACAAAAATTCCACAAAAATTCCACAAAAATTCACAAAAATTCCACAAAAATTCACAAAAATTCAAAAATTCAAAAATTCCACCCTGAAGAATCTTAGTTAAAAATTCAAGAA  Qy 2164 GGTCTGCCAACACAAAAAATGACTCCAAAAAATCAAAATCCAAGAATCTTAGTTACAAAATTTCAAGAA  Qy 2264 TCATTCGGGACTTCTGAGAAAATGACTCCAAAAAATCAAAATCAAAAATCAAAAATCAAAAATCAAAAAA
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                                                                                                                                                                                                         Cowell, J.K. and Kaye, F.J.

Partial inactivation of the RB product penetrance of familial retinoblastoma a oncogene 9 (5), 1321-1326 (1994)
                                                                                                                                                Mutation data provided by Dr. Hospital for Sick Children 555 Univ. Ave.
                                                                                                                                                                                                                                                                                                                               Hogg, A., Bia, B., Onadim, Z. and Cowell, J.K.
Molecular mechanisms of oncogenic mutations in tumors from
with bilateral and unlateral retinoblastoma
Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onadim, Z., Hogg, A., Baird, P.N. and Cowell, J.K. Oncogenic point mutations in exon 20 of the RB1 gene showing incomplete penetrance and mild expression of
                                                                                                                                Toronto ONT W5G
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1 ATGGAGAAAGTTTOATTOATT 821193 segs, -1518192014 residues OLIGO\_NUC February 13, 2000, 11:20:43; Search time 14294,3 Seconds (without alignments)
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## SUMMARIES

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 105311 LOCUS DEFINITI	. <del>ф.</del> ў	442	40 40	37 38	36	1 U U	310		27	4 12 C	223	222	219	17 18	115	13	12	10	ი ად <b>-</b>	10	<b>∪</b> 1 •⊳	ωι		Result	
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Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
Detection of heterozygous mutations in the AB1 gene in
retinoblastoma patients using single-strand conformation
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Oncogene 7 (7), 1445-1451 (1992)
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Structure and partial genomic
susceptibility gene
gene 80 (1), 119-128 (1989)
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   mutation data provided by Dr. B.L.Gallie, Hospital for Sick Children 555 Univ. Ave.
                                                                         Kratzke,R.A., Otterson,G.A., Hogg,A., Coxon,A.B., Geradts,J., Cowell,J.K. and Kaye,F.J.
Partial inactivation of the RB product in a family with incomplete penetrance of family retinoblastoma and benign retinal tumors oncogene 9 (5), 1321-1326 (1994)
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Molecular mechanisms of oncogenic mutations in tumors f
with bilateral and unilateral retinoblastoma
proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
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## GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

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### SUMMARIES

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Patent: EP 0259031-A2 1 09-MAR-1988;
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2043	antatagaccttaaattcaaaatcattgtaacagcatacaaggatcttcctcatgctgtt	1984	VΩ
2145	AGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAG	2086	đđ
	NCAGGCATTTGGACCAAATTATGATGTGTTTCCATGTATGGCATATGCAAAGTGAA	io.	γр
2085	TAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCA	2026	ф
1923	TCCAGCACACCCTGCAGAATGAGTATGAACTCAT	m	Qγ
2025	CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAAACGCCTTCTGTGTGAGCACCCAGAA	1966	da
1863	GGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCCTTCTGTCTG	1804	Qy
1965	TTCCAGACCCAGAAGCCATTGAAATCTACCTCTTTTCACTGTTTTATAAAAAAGTGTAT	1906	40
1803	CCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAAGTGTA	1744	γ
1905	AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAGCC	1846	qq
1743	STTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCA	1684	Οу
1845	CTCCAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAA	7	da
1683	CAGAATAATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAG	62	Ωу
1785	TCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTTCTTTAATCTTCCT	7	đđ
1623	CAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCTGCTTGTCCTCTTTAATCTTCCT	1564	Qy
1725	CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA	1666	da
1563	AATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTGATCTTATTAAACAA	50	Ωу
1665	ATCAAAGCAGAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT	1606	da
1503	PAGAAGGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGTGAACAT	4.4	ΩУ
1605	TGGATTCTGAATGTGCTTAATTTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTT	1546	aa
1443	GATTCTGAATGTGCTTAAATTTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTT	38	φ
1545	GCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCA	1486	σα
	ATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCC	N	Qy
1485	CTTCTGAATGACAACATTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAATG	4	dd
1323	SAATGACAACATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTGTAAT	6	Qy
1425	GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAA	1366	gg
1263	TAATGGAATCCATGCTTAAATCAGAAGAAGAAGAACGATTATCCATTCAAAATTTTTAGCAAA	20	γо
1365	GAGTTCGCTTGTATTACC	1306	ф
1203	GGTTGTGTCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGA	1144	Ωу
1305	NAATTTGCTAAAGCTGTGG	1246	ממ
1143	TGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTTGCTAAAGCTGTG	1084	Qy
1245	TCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG	1186	ф
1083	CTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG	1024	Qy
1185	GAACACTATCCAACAATTAATGATGATTTTAAAT!	1126	da
1023	IGITATGAACACTATCCAACAATTAATGATGATTTTAAATTCAGCAAGTGATC	964	Qy
1125	GGTGAATGTAATTCCTCCACACACTCCAGT	1066	рb
963	CCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAG	904	Qy

Oy  64 TRACTIGGGACIAMOSTITCANCIGGAGGASTATIGGGAGGATATATIGGAAGAAAAAAAAAA	Db 304 GATTTTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAG	GATITTACTGCATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAG	Query Match 99.9%; Score 2619; DB 5; Length 2994; Best Local Similarity 100.0%; Pred. No. 0; Matches 2619; Conservative 0; Mismatches 0; Indels 0; Gans 0;		<pre>TITLE Characterization of a novel anti-p110.sup.RB monoclonal antibody JOURNAL Patent: US 5710255-A 2 20-JAN-1998; FEATURES tocation/Qualifiers</pre>		GI:3209762		11111111111111111111111111111111111111			2566 GACCOTTGAATATTGAAGGATCAGATGAAGCAAGCTAAACCACTCCCAGGAGAGTCCC		TORGER OF THE CONTROL OF THE CONTR	CCCTTACGGATTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATT		OV 2164 CCCCCTACCTGCACCAATACCTCACACTTCCTCGAAGCCCTTTACAAGTTTCCTACGTTCACCACTACAACTTCTTACTTCACCACCTACCT		Db 2146 AATATAGACCTTAAATTCAAATCATCAAAGAAGAAGAAGAATCATCTCTCTC
TIGGGAGAAAGTTTCATCTGTGGATGGATTATGGGAGGTATTCATATTCA TIGGGAGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATTTCA TIGGGAGAAAGTTTCATCTGTGATGAAATTCAGTTGACCTAGATTGAGTT  **CTGTGGGGGAATCTGTATCTTTATTGCAGCAGTTATTCAGT **CTGTGGGGGAATCTGTATCTTTATTGCAGCAGTTATTCAGT **CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTATTCAGT **CTGTGGGGAATCTGTACCAAAAGATTGTGAAATTCTTTAAAATTCAGTTGAAATTCTTTAAAATTCAGTTGAAATTCTTTAAAATTCAGTTGAAATTCATTTAAAATTCAGTTGAAATTCAGTTGAAATTCAGTTGAAATTCATTTAAAATTCAGTTGAAATTCTTTAAAATTCAGTTGAAAATTAGAATTCAGTAGAATTCAGTAGAATTCAGTAGAATTAGAATTCAGTAGAATTAGAATTCAGTAGAATTAGAATTCAGTAGAATTAGAATTCAGTAGAAATTAAAACTTCAGAAAGTTGAAAATTAAAACTTCAGAAAGTTAAAACTTCAGAAAGTTAAAACTTCAGAAAGTTTAAAACTTCAGAAAGTTAAAACTTCAGAAAGAA	1144	1084	1024 1324	964 1264	904 1204	844 TTTT      1144 TTTT	784 AATC	724 TTT#      1024 TTT#	664 GTTC      964 GTTC	604 GGTC     904 GGTC	544 AAAG       844 AAAG	484 TTTC      784 TTTC	424 ATC	364 CAAC      664 CAAC	304 GATG	244 AAAC      544 AAAC	184 ACTT {    484 ACTT	124 AAGG {    424 AAGG	64 TTA/      364 TTA/
그림 남그님 뭐그림 말그림 당그의 요구요 요구요 장구랑 방그병 남그림 오구오 방그림 방그림 병그림 청구절 청구절 청구절 하고의 네크리 원구원	angacheaaggafataggatacatctttaaagagaaatttgctaaag ttgtgtcgaaattggatcacagcgatacaaacttggagttcgcttgt	AGAGTGAÁGGATATAGGATACATCTTTAAAGAGAGAAATTTGCTAAAG 	ngaaaatctgatttcctattttaacaactgcacagtgaatccaaaag 	IGTTATGAACACTATCCAACAATTAATGATGATTTAAATTCAGCAA 	rcgaaaaagtaaccttgatgaagaggtgaatgtaattcctccacaca 	3GATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAA 	ITCTAAACGATÁCGAAGAAATTTATCTTAAAAATAAAGATCTAGATG 	acctttatgaattctcttggacttgtaacatctaatggacttccag. 	CTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAAÌGTTTATT 	GAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAA 	accatataaaacagctgttatacccattaatggttcacctcgaacac 	GTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCA 	attitatiagciaaagggbagtatiacabatggbagatgatctgg 	CAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAG 	attgtttgcactcttcagcaaattggaaaggacatgtgaacttatat 	rattgataccagtaccaaagttgataatgctatgtcaagactgttga 	TACTGAGCTACAGAAAACATAGAAATCAGTGTCCATAAATTCTTTA 	actgtggggaatctgtatctttattgcagcagttgacctagatgaga 	TIGGGAGAAAGITICAICIGIGGAIGGAGIAIIGGGAGGITAIAITC 

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                                                                                                                                                                                                                                                                                                         Hogg.A., Onadim.z., Baird.P.N. and Cowell.J.K.
Detection of heterozygous mutations in the RB1 gene in retinoblastoma patients using single-strand conformation polymorphism analysis and polymerase chain reaction seque oncogene 7 (7), 1445-1451 (1992) 92319557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMRBIMRNA
Homo sapiens
mutations.
                                                                                                                                                                                                                                                                                                                                                                                                          NCGeeT.L., Yandell,D.W. and Dryja,T.P. Structure and partial genomic sequence of the human susceptibility gene Gene 80 (1), 119-128 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens cDNA to mRNA.
Homo sapiens
Eukarrota
                                                                                                                                                                                                                    3 (gites)
3 (gites)
6 Onadim, Z., Hogg, A., Baird, P.N. and Cowell, J.K.
6 Oncogenic point mutations in exon 20 of the RB1 gene
8 showing incomplete penetrance and mild expression of
7 retinoblastoma phenotype
8 Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (199
                                                       HoggyA., Bia,B., Onadim,Z. and Cowell,J.K.
Molecular mechanisms of oncogenic mutations in tumors
with bilateral and unilateral retinoblastoma
proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
                                                                                                                                              Onadim, Z., Hogg, A. and Cowell, J.K.
Mechanisms of oncogenesis in patients with familial retinoblastoma
Br. J. Cancer 68 (5), 958-964 (1993)
Kratzke, R.A., Cowell, J.K. a
                                            93348271
                                                                                                                                    94031584
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Eutheria; Primates; Catarrhini; Hominida
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 Otterson, G.A., nd Kaye, F.J.
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                Hogg, A., Coxon, A.B., Geradts, J.,
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gb_pr2:HUMRBSY79

gb_pat:109384

gb_pi1:HUMF
   gb_pat:109386
gb_pr1:HUMRBS08
gb_pr1:HUMRBS07
gb_pr2:HUMRB08EX
gb_pr1:HUMRB525EX
gb_pr2:HUMRB1510K
gb_pr2:HUMRB1510K
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9b_pat:109389
9b_pr1:HUWRB820
9b_pr2:HUWRB4MU2
9b_pr2:HUWRB1777L
9b_co:RAFRINBL67
9b_pr2:HUWRB17MU2
9b_pr2:HUWRB17MU2
9b_pr1:HUWRB18
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9b_pat:118496
9b_pat:118497
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9b_pat:HUMRBS
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gb_pr1:HUMRETBLAS
gb_ro:RATRP
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-MODEL-frame+_D2n.model -DEV-xlp
-Q-/Ggn2_1/USPT0_Spool_VGS09026459/runat_12022000_171247_15926/app_guery.fasta.1
-Q-/Ggn2_1/USPT0_Spool_VGS09026459/runat_12022000_171247_15926/app_guery.fasta.1
-DB-GenEmb1 -QFMT-fastap -SUFFIX-0ligo.rge -GAPOD=4.500
-GAPOD=0.000 -MINAATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOD=4.500 -QGAPEXT=0.050 -XGAPOD=60.000 -XGAPEXT=60.000
-FGAPOD=6.000 -FGAPEXT=7.050 -YGAPOD=60.000 -YGAPEXT=60.000
-FGAPOD=6.000 -DELEXT=7.000 -YGAPOD=60.000 -YGAPEXT=60.000
-DELDQ=6.000 -DELEXT=7.000 -START=1 -MATRIX-01igo
-TP-MG-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-quality
-TR-MG-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-quality
-TR-MG-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-quality
-TR-MG-human40.cdi -MSD=LCCAL -OUTFMT=pfs -NORM-ext -MINLEN-0
-MS_MS_M=1000000 -USER-US09026459 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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gb_pat:I09377
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gb_pat:181465
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Database length: ~1518192014
Search time (sec): 10867.920000
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gb_pat:I09373
gb_pr1:HUMRBS04
gb_pr2:HUMRB04MUT
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US-09-026-459A-35 x I05311
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LOCUS 105311
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Ratio: 1.000
Percent Similarity: 100.000
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135 roproMetLeuLeuLysGluProTyrLysThrAlaValIleProIleAsn
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                                                                                                                                                                                                             492 ATTGGAAAGGACATGTGAACTTATATTTGACACAACCCAGCAGTTCGA
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                                                           eSerPheGlnLeuMetLeuCysValLeuAspTyrPheIleLysLeuSerP
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Dryja,T.P. and Friend.S.
Human DNA in the diagnosis of retinoblastoma
Patent: EP 0259031-A2 1 09-MAR-1988;
Docation/Qualifiers
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2392 CGGATTCCTGGAGGAACATCTATATTTCACCCTGAAGAGTCCATATAA 2441 718 SILESECGIUGLYLEUPTCThrIPTCACCCTGAAGAGTCCATATAA 2441 718 ATTTCAGAAGGTCTGCCAACAACAACAAAAATGACTCCAAGAACAAGAACAACAAAAAATGACTCCAAGAACAAGAACAACAAAAAATGACTCCAAGAACAAGAACAACAAAAAATGACTCCAAGAACAACAAAAATGACTCCAAGAACAACAAAAATGACTCCAAGAACAACAAAAATGACTCCAAGAACAACAAAAATGACTCCAAGAACAACAAAAATGACTCCAAGAACAACAAAACAAAATGACTTCTGAGAAAGTTCCAAGAAA 2541 2492 TCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAAGTTCCAGAAA 2541	2242 GAGTATGATTATTAGTATTGTTATAACTCGGTGTCTCAGCAGAACT 2291 668 ULYSThrAsnIleLeuGlnTyrAlaSerThrArgProProThrLeuSerP 685	22 AGGCATTTGGACCAAATTATGATGTTCCAAGTTTTTTTTT		SHISLEUG

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Similarity:
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Unclassified.
1 (bases 1 to 2994)
3 (bases 1 to 2994)
5 Shepard, H. Michael and Wen, S. Fen.
Characterization of a novel antiplio.sup.RB mor
Characterization 2 20-JAN-1998;
Location/Qualifiers
2994
leSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
                                                      sLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSerI
                                  ATTGGAAAGGACATGTGAACTTATATTTTGACACAACCCAGCAGTTCGA
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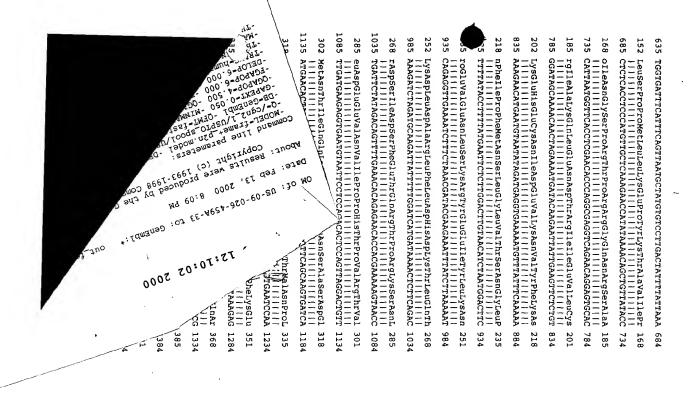
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LOCUS HUMRBIMRNA 4839 bp mRNA
DEFINITION Homo sapiens retinoblastoma susceptibility protein (RB1) mRNA
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                                                                                                                                                                                                                              Hogg, A., Onadim, Z., Baird, D.N. and Cowell, J.K.
Detection of heterozygous mutations in the RB1 gene in
retinoblastoma patients using single-strand conformation
polymorphism analysis and polymerase chain reaction seque
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ACTAGAGGAGTATGATTATATAGTATTCTATAACTCGGTCTTCATGC
                       sGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPheMetG
                                                                   LysaspLeuProHisAlaValGlnGluThrPheLysArgValLeuIleLy
                                                                                                                  TANATACACTTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACAT
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                                                          AAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAA
                                                                                                      GCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATAC
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                                                                              Hogg,A., Onadim,Z., Baird,P.N. and Cowell,J.K. Detection of heterozygous mutations in the RBI gene in retinoblastoma patients using single-strand conformation polymorphism analysis and polymerase chain reaction seque Oncogene 7 (7), 1445-1451 (1992)
Onadim, Z., Hogg, A., Baird, P.N. and Cowell, J.K. Oncogenic point mutations in exon 20 of the RBI gene showing incomplete penetrance and mild expression of retinoblastoma phenotype Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (199
                                                                                                                                                                                Structure and partial genomic sequence of the human susceptibility gene Gene 80 (1), 119-128 (1989) 90006771
                                                                                                                                                                                                                                                                                                         L41870.1 GI:793994 retinoblastoma susceptibility Homo sapiens cDNA to mRNA.
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1 (RB1) mRNA
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Ratio: 1.000
Percent Similarity: 100.000
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                               802 IleGluGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSe 818
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                                                                                                                                                                423 AAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATG
   68 pAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAlaLeuP 85
                                                                                                                                                                                  18 sLysGluLeuTrpGlyIleCysIlePheIleAlaAlaValAspLeuAspG 35
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l (bases 1 to 2994)
Shepard, H.Michael and Wen, S.Fen.
Characterization of a novel anti-pil0.sup.RB monoclonal antibody
Patent: US 5710255-A 2 20-JAN-1998;
Paccation/Qualifiers
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Sequence 2 from patent US 5710255.
I81465 GI:3209762
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368 gTyrLysLeuGlyValArgLeuTyrTyrArgValMetGluSerMetLeuL 385
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268	LysaspLeuAspalaargLeuPheLeuAspHisAspLysThrLeuGlnTh	252
1172		1123
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502 1735	ArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuPr 518	
518 1785	oLeuGlnAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgS 535 	
535 1835	erProLysLysGlySerThrThrArgVallAsnSerThrAlaAsnAla 551	
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718 2385	rProLeuArgI1eDroGlyGlyAsnIleTyrI1eSerProLeuLysSerP 735 	
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9b_un:M27861

9b_pat:109377

9b_pat:109386

9b_pr1:HUMRBS08

9b_pr1:HUMRBS17

9b_pr2:HUMRB0825

9b_pr1:HUMRB522

9b_pr1:HUMRB5523

9b_pr2:HUMRB1610K

9b_pr2:HUMRB151MUT
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Database length: -1518192014
Search time (sec): 10867.920000
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Query: US-09-026-459A-33
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            197 | 105311 Sequence 1 from Patent 194 | 181465 Sequence 2 from patent 189 | 141870 Homo sapiens retinoblastoma 294 | M33647 Human retinoblastoma 294 | M28419 Human retinoblastoma 295 | 118496 Sequence 1 from patent 297 | 109369 Sequence 2 from patent 297 | 118497 Sequence 2 from patent 297 | 109369 Sequence 1 from patent 297 | 109369 Sequence 2 from patent 297 | 109369 Sequence 1 from patent 297 | 109369 Sequence 2 from patent 297 | 109369 Sequence 2 from patent 297 | 109369 Sequence 1 from patent 298 | 11910 Human mutated retinoblast 298 | 1211910 Human retinoblastoma 2016 | 125233 Rat mRNA for retinoblastoma 2016 | 125233 Rat mRNA for retinoblast 2016 | 125233 Rat mRNA for retinoblas
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gb_pat:109373
gb_pr1:HUWRBS04
gb_pr2:HUWRBO4MUT
gb_pr2:HUWRB19MUT
gb_pr2:HUWRB20MUU
gb_pat:109385
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AUTHORS
TITLE
JOURNAL
FEATURES
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ACCESSION
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KEYWORDS
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ORGANISM
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US-09-026-459A-33 x I05311
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Dryja,T.P. and Friend,S.
Human DNA in the diagnosis of retinoblastoma
Patent: EP 0259031-A2 1 09-MAR-1988;
Location/Qualifiers
1. .4597
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# GenCore version 4.5 Copyright (c) 1993 - 1998 Compugen Ltd.

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KEYWORDS SOURCE ORGANISM	RESULT 1 105311 LOCUS DEFINITION ACCESSION VERSION		4 4 4 51 4 W																							ю <b>-</b>		Result	
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	02-DEC-1994		109382 Sequence 15 M27856 Human retin L49222 Homo sapien	des	M27859 Human retin	L41996 Homo sapien	L41999 Homo sapien	sapie	L41896 Homo sapien	I09377 Sequence 10	M27860 Human retin	L49225 Homo sapien	L35147 Human retin	ဂ္ဂဇ္ဇ	L49230 Homo sapien AF043224 Homo sapi	L41910 Homo sapien	109389 Sequence 22	L49220 Homo sapien	M27858 Human retin	M19701 Human mutat I09384 Sequence 17	A01444 H.sapiens D	<pre>109369 Sequence 1 M15400 Human retin</pre>	Human	L41870 Homo sapien M33647 Human retin	I18497 Sequence 2 I81465 Sequence 2	118496 Sequence 1	dtros		

REFERENCE AUTHORS

Unknown.
Unknown.
Unclassified.
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1 (bases 1 to 4597)
Dryja,T.P. and Friend,S.

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0;	uery Match 100.0%; Score 2343; DB 5; Length 4597; sest Local Similarity 100.0%; Pred. No. 0; faps datches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps	Que Bes Mat
	TITLE Human DNA in the diagnosis of retinoblastoma JOURNAL Patent; EP 0259031-A2 1 09-MAR-1988; FEATURES Location/Qualifiers Source 1.4597 ASE COUNT 1489 a 842 c 812 g 1454 t PRIGIN	TI: JOI FEATI BASE ORIGI

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1920	TTTTGCAGTATGCTTCCACCAGGCCCCCTACCTTGTCACCAATACCTCACATTCCTCG	1861	Ωу
1860 2301	GAGTATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGAGACTGAAAACAAT	1801	. <b>Q</b>
1800	TACAAGGATCTTCCTCATGCTGTTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAG	1741 2182	p dy
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1680	TGCAGAATGAAGTATGAAGTCAGAGAGAGAGAGAGAGAGA	ກໍ່	Ş
1620 2061	CGCCTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCC	1561 2002	70 AG
2001	CACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTG	1942	Dδ
1560	TCACTGTTTTATAAAAAGTGTATCGGGCTAGCCTATCTCCGGGCTAAATACACTTTGTGAA	Ç	Qy
1941	GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTC	1882	뫋
1500	CAGAGACAC	1441	Qy
1881	Ž.	1822	фd
1440	CTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTACT	1381	Qy
1821	AATCACACTGCAGCAGATATGTATC	1762	뭥
1380	CTGCTTGTCCTCTAATCTTCCTCTCCAGAATAATCACACT		Qy
1761	CCTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAA	1702	ф
1320	CTTTATTTGATCTTATTAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCT	1261	Qy
1701	CGAATCATGGAATCCCTTGCATGGCTCTCAGATTC	1642	đđ
1260	AACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGG	1201	Qy
1641	AAGGCAACTTGACAAGAGAAATGAT	1582	рb
1200	TTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGC	1141	Qy
1581	ATTCTGAATGTGCTTAATTTAAAAGCCTTTGA	1522	Дb
1140	CTGGAACAGATTTGTCTTTCCCATGGATT	1081	Qy
1521	GCGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT	1462	ф
1080	CGTGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCT	0	Q
1461	TTATCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTG	1402	дb
1020	TATCCATTCAAAATTTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTI	961	Qy
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960	TTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGA	901	ОУ

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1981 CCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCCAACACCAACAACAATGACTCCA 2040

Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  4 ATGTCAAGACTGTTGAAGAAGTATGATGATGTTTGGACTCTTCAGCAAATTGGAAAGG 60  124 ATGTCAAGACTGTTGAAGAAGTATGATGTTTTTTTTTTGACTCTTCAGCAAATTGGAAAGG 60  125 ATGTCAAGACTGTTGAAGAAGTATGATGTTTTTTTTTTGACTCTCAGCAAATTGGAAAGG 183  Qy 61 ACATGTGAACTTATATATTTGACACCAAGCGAGGTTCGATATCTACTGAAAATTGT 120  1111111111111111111111111111111111	RESULT 2 118496	Db 2422 CCCCTGAAGATCTTAGTATCAATTGGTGAATCATCGGGACTTCTAGAAGAGTCCAGAAA 2100  Qy 2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2100  Qy 2041 AGATCAAGAATCTTAGTATCAATTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAA 2541  Qy 2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAAGAAGTTCCAGAAA 2541  Qy 2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTTCCAGAAA 2541  Qy 2101 ATAAATCAGATGGTATGTAACAGCGACCGTGTGCTCAAAAGAAGTGCTGAAGGAAG
Oy 1021 GCGTGCGCTCTTGAGGTGAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGAT 1080	721 AUTTTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTTAACAACTGC	Oy  301 GGTTCACCTCGAACACCCAGGCGAAGGTCAGAACAGGATAGCAAAACAACTA 360

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100.0%; Score 2343; DI
Similarity 100.0%; Pred. No. 0;
$3; Conservative 0; Mismatches
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iu,H., Hu,S. and Benedict,W.F.
sroad-spectrum tumor suppressor genes, gene products and methods
for tumor suppressor gene therapy
Patent: US 5496731-A 2 05-MAR-1996;
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TTAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGC
                                                                                                                        GACAGTTTTGAAACACAGAGAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAAT
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9b_pr1:HUMRBS20
9b_pr2:HUMRB23EX
9b_pr2:HUMRB4MU2
9b_pr2:HUMRB1777L
9b_pr3:AF043224
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gb_pr2:HUMRBANNA
gb_pr2:HUMRBANA
gb_pr2:HUMRBSA
gb_pr2:HUMRBSA
gb_pat:109369
gb_pat:401444
gb_pat:A01444
9b_pat:109386
gb_pr1:HUMRBS08
gb_pr1:HUMRBS19
gb_pr2:HUMRBS19
gb_pr2:HUMRB522
gb_pr2:HUMRB25EX
gb_pr2:HUMRB1610K
gb_pr2:HUMRB17MUT
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9b_pr2:HUMRB17MU2
9b_pat:I09387
9b_pr1:HUMRBS18
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Query: US-09-026-459A-37
Query length: 781
Database: GenEmbl:*
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Database length: -1518192014
Search time (sec): 10867.920000
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gb_pat:I18497
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-Q-/Ggn2_1/USPTO_spool/US99026459/runat_12022000_171247_15926/app_query.fasta.
-Q-/Ggn2_1/USPTO_spool/US99026459/runat_12022000_171247_15926/app_query.fasta.
-QB-GenEmbl -QFMT-fastap -SUFFIX-voligo.rge -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPELT=0.000 -LOOPEXT=0.000
-QGAPEXT=0.050 -MINMATCH=0.100 -VGAPEXT=60.000
-YGAPEXT=60.000
-YGAPEXT=7.000 -YGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000
-DELOP=6.000 -DELXT=7.000 -START=1 -MATRIX=011g0
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THA_VN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-MAIN-1000000 -USER-US09026459 -NCPU=6 -ICPU=3 -NO_XLPXX -WAIT
-TH. DS=1
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1 118496 Sequence 2 from patent
1 118497 Sequence 2 from patent
1 181465 Sequence 2 from patent
1 181465 Sequence 2 from patent
1 141870 Homo sapiens retinobla
1 M33647 Human retinoblastoma a
1 M28419 Human retinoblastoma a
2 M28419 Human retinoblastoma a
2 109369 Sequence 1 from Patent
3 109369 Sequence 1 from Patent
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                                     47 Human retinoblastoma sus
25 Homo sapiens retinoblast
61 Figure 2. Retinoblastoma
77 Sequence 10 from Patent
86 Sequence 19 from Patent
46 Human retinoblastoma sus
60 Human retinoblastoma sus
96 Homo sapiens retinoblast
12 Homo sapiens retinoblast
12 Homo sapiens retinoblast
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gb_pr2:HUMRB19MUT
gb_pr2:HUMRB20MUU
gb_pat:109385
gb_pr1:HUMRB816
gb_pr2:HUMRB81646F
gb_pr2:HUMRB1646F
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US-09-026-459A-37 x I05311
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                   TTTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGAT
isGluCysAsnIleAspGluValLysAsnValTyrPheLysAsnPheIle
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Dryja.T.P. and Friend.S.
Human DNA in the diagnosis of retinoblastoma
Patent: EP 0259031-A2 1 09-MAR-1988;
Location/Qualifiers
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4.9e-33
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Quality: 781.00
Ratio: 1.000
Percent Similarity: 100.000
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US-09-026-459A-37 x I18496
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           117 aLysGlnLeuGluAsnAspThrArgIleIleGluValLeuCysLysGluH 134
                                                                                                      324 TTCATTTCAGTTAATGCTATGTGTCCTTGACTATTTTATTAAACTCTCAC 373
                                                                                                                                                                                                                                                                        224 TATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA 273
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                                                 AMAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTAAAGAAC
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Xu,H., Hu,S. and Benedict,W.F.

Broad-spectrum tumor suppressor genes, gene products and methods for tumor suppressor gene therapy patent: US 5496731-A 1 05-MAR-1996;
Location/Qualifiers
1. 3232
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Unclassified.
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Sequence I from patent US 5496731.
I18496 GI:1598851
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Percent Identity: 100.000
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450	${\tt lyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln}$	434
434 1423	USERASPSERFICEUPheAspLeuIleLysGlnSerLysAspArgGluG	417 1374
417 1373	LysHisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLe	401 1324
400	allleGluSerPheIleLysalaGluGlyAsnLeuThrArgGluMetIle	384
1323		1274
384 1273	eProTrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysV 	1224
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1223		1174
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1173		1124
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1123		1074
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1073		1024
300 1023	laLysAlaVaiGlyGlnGlyCysValGluIleGlySerGlnArgTyrLys	284 974
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973		924
267	GluasnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSe	251
923		874
250	hrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnDroSer	234
873		824
23 <b>4</b>	ugluvalasnvalileproprohisthrprovalargThrvalmetAsnt	217
823		774
217 773	IleaspSerPheGluThrGlnArgThrProArgLysSerAsnLeuAspGl	201 724
200	euAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer	184
723		674
184	IGluasnleuserlysargTyrGluGluIleTyrLeulysasnlysaspl	167
673		624
167	ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluVa	151
623		574
150	isGluCysasnIleAspGluValLysAsnValTyrPheLysAsnPheIle	134
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                                      AATTTCAGAAGGTCTGCCAACACCAACAAAATGACTCCAAGATCAAGAA
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                                                                                                         IleAsnGlnMetValCysAsnSerAspArgValLeuLysArgSerAlaGl
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US-09-026-459A-37 x I18497/rev
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TITLE
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Xu,H., Hu,S. and Benedict,W.F.
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1470. .1526
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/citation=[5]
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ON Human retinoblastoma associated (RBI) mRNA, complete cds.

N M33647.1 GI:190945
retinoblastoma protein.
Homo sapiens (clone: p4.7R) cDNA to mRNA.

SM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Memmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 4600)
S Friend, S. H., Horowitz, J. M., Gerber, M. R., Wang, X. F., Bogenmann, E., Li, F. P. and Weinberg, R. A.
Deletions of a DNA sequence in retinoblastomas and mesenchymal tumors: organization of the sequence and its encoded protein [published erratum appears in Proc Natl Acad Sci U S A 1988]

Apr. 87(7), 79241
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Human DNA in the diagnosis of retinoblastoma

Human EP 0259031-A2 1 09-MAR-1988;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4600)

Friend.S.H., Horowitz,J.M., Gerber,M.R., Wang,X.F., Bogenmann,; Li,F.P. and Weinberg,R.A.

Deletions of a DNA sequence in retinoblastomas and mesenchymal tumors; organization of the sequence and its encoded protein [published erratum appears in Proc Natl Acad Sci U S A 1988]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMRBAlRA 4600 bp mRNA PRI
Human retinoblastoma associated (RB1) mRNA,
M33647 J02994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry and computer-readable copy of sequence for [1] kindly
led by S.H.Friend, 10-FEB-1988.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A. 84 (24), 9059-9063 (1987)
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ORIGIN
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KEYWORDS SOURCE

VERSION

2890

885

868

2690

835

818

о 51

2640

802

2590

785

REFERENCE

TITLE AUTHORS

JOURNAL MEDLINE COMMENT

FEATURES

gene

CDS

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1489 b

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alignment_block:
US-09-026-459A-29 x HUMRBAlRA
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AspG1yValLeuG1yG1yTyrI1eG1nLysLysG1uLeuTrpG1yI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AACAGAAGAACCTGATTTTACTGCATTATGTCAGAAATTAAAGATACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 hrGluLeuGlnLysAsnIleGluIleSerValHisLysPhePheAsnLeu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 spHisValArgGluArgAlaTrpLeuThrTrpGluLysValSerSerVal
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                                                                                                                 aLysGlyGluValLeuGlnMetGluAspAspLeuValIleSerPheGlnL
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                                                                                                                                                                                                                                                                                                  hrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGlu
                                                                                                                                                                                                                                                                                                                                                                                     uLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uThrGluGluProAspPheThrAlaLeuCysGlnLysLeuLysIleProA 35
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768 yGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluG 785	2 IleproArgSerProTyrLysPheProSerSerProLeuArgIleproIlell	5 leLeuGlnTyrAlaSerThrArgProProThrLeuSerProIleProHis 75	73	702 ValGlnGluThrPheLysArgValLeuIleLysGluGluGluTyrAspSe 718	185 spleulysPhelysIleIleValThrAlaTyrLysAspleuProHisAla 70 	668 pGlnrleMetMetCysSerMetTyrGlyrleCysLysValLysAsnrleA 685 [	652 GINHISThrLeudlnasnGluTyrGluLeuWetargAspArgHisLeuAs 668	5 rgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPhe 	618 rLystysValTyrArgLeuAlaTyrLeuArgLeuAsgThrLeuCysGluA 635	ysProLeuLysSerThrSerLeuSerLeuPheTy 6 	585 erThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 601	568 rAlaālaaspmetTyrLeuSerProValArgSerProLysLysClys 585 	552 HisLeugluSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHisTh 568 [	535 roleuPheAspLeuIleLysGlnSerLysAspArgGluGlyProThrAsp 551	518 uArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerP 535	502 PhelleLysalagluGlyAsnLeuThrArgGluMetIleLysHisLeuGl 518	485 euasnvalleuasnleulysalapheasppheTyrtysvallleGluSer 501	

TACATOTOAGAATOTTGATTOTGGAACAGATTTGTCTTTCCCATGGATTC 1689 rThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleL 485  

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ACCESSION
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The retinoblastoma susceptibility gene encodes a nuclear phosphoprotein associated with DNA binding activity Nature 329 (6140), 642-645 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M28419.1 GI:190962 retinoblastoma susceptibility protein Homo sapiens retinoblastoma cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2994)

Lee.W.H., Shew.J.Y., Hong, F.D., Sery, T.W., Donoso, L.A., Young, L.J.,

Bookstein, R. and Lee, E.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note-"retinoblastoma suceptibility protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MIC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA PRI 12-JUL-1995 susceptibility protein mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2705
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US-09-026-459A-29 x HUMRBSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 894.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLe 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 IleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrCysGluLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGlu 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTA 490
  luAsnAspThrArgIleIleGluValLeuCysLysGluHisGluCysAsn
                                                                                                                                                       CTCAAAGAACCATATAAAACAGCTGTTATACCCCATTAATGGTTCACCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  974
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a 618 c 59:
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KEYWORDS SOURCE

VERSION

FEATURES

CDS

TITLE

AUTHORS

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RVLKRSAEGSNPPKPLKKLRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ
809 t
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Percent Identity: to: 2994 894 0 100.000

CTGAGCTACAGAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTA hrGluLeuGlnLys&snIleGluIleSerValHisLysPhePheAsnLeu 101 540

uLeuLysLysTyrAspValLeuPheAlaLeuPheSerLysLeuGluArgT 135 CTAAAAGAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACT

590

GTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAGCAAATTGGAAAGGA 640

740

840 201

LeuLysGluProTyrLysThrAlaVallIeProIleAsnGlySerProAr 218 890

gThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuG 940 235

906 TYCTCTTCGACTTGTAMCATCTANTGACTTCCAGAGGTTGAMAATCTTT 955  917 GELYBACGTTGGUGLULLETYLEULYSASHLYSASPLEABAPAT 301  1011   1111   1	202 LeuLysGluProTyrLysThrAlaVallleProIleAsnGlySerProAr 218
585 erThrThrargValasnsorThrAlasnalaGluThrGlnAlaThrSer 601 11111111111111111111111111111111111	

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801	lyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSer	785
2505		2456
785	yGlyasnileTyrileSerProLuLysSerProTyrLysIleSerGluG	768
2455		2406
768 2405	IleProArgSerProTyrLysPheProSerSerProLeuArgIleProGl	752 2356
751 2355	leLeuglnTyrAlaSerThrArgProProThrLeuSerProTleProHis	735 2306
735	IlelevalPheTyrAsnSerValPheMetGlnArgLeuLysThrAsnI	718
2305		2256
718	ValgingluthrpheLysargValLeulleLysGluGluGluTyraspSe	702
2255		2206
701 2205	SpleuLysPheLysIleIleValThrAlaTyTLysAspLeuProHisAla	685 2156
685	pGlnIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleA	668
2155		2106
668	GlnHisthrLeuglnasnGluTyrGluLeuMetArgAspArgHisLeuAs	652
2105		2056
651	rgLeuLeuSerGluHisProGluLeuGluHisIleIleTrpThrLeuPhe	635
2055		2006
635	rlyslysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluA	618
2005		1956
618	AlapheGlnThrGlnLysDroLeuLysSerThrSerLeuSerLeuDheTy	602
1955		1906
1905	erThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSer 	585 1856
585 1855	TAlaalaaspMetTyTLeuSerProValArgSerProLysLysClysClysClysClysClysClysClysClysClysCl	568 1806
568	HisteugluSeralaCysbroLeuAsnLeuProLeuGlnAsnAsnHisTh	552
1805		1756
551 1755	roleuPheAspleuIleLysGlnSerLysAspArgGluGlyProThrasp	535 1706
535	uArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerP	518
1705		1656
1655		1606